3. The method of claim 1, wherein two or more haplotypes are determined.

4. The method of claim 1, wherein the genetic locus is an HLA locus.

5. The method of claim 1, wherein the at least one haplotype is associated with a genetic disease.

6. The method of claim 5, wherein the disease is cystic fibrosis.

7. The method of claim 5, wherein the disease is phenylketonuria, muscular dystrophy or beta-thalassemia.

8. The method of claim 1, further comprising forensic testing.

9. The method of claim 8, further comprising:

   (a) analyzing DNA from a crime scene sample;

   (b) analyzing DNA from a sample of a suspected perpetrator of the crime; and

   (c) comparing the haplotypes present in the crime scene sample and the suspected perpetrator sample.

10. The method of claim 1, further comprising paternity testing.

11. The method of claim 10, further comprising:

   (a) analyzing DNA from an off-spring;

   (b) analyzing DNA from at least one suspected parent; and

   (c) comparing the haplotypes present in the offspring's DNA and in the suspected parent's DNA.

12. The method of claim 1, wherein the amplified genomic DNA further comprises at least part of at least one exon.

13. (Amended) A method for determination of at least one haplotype of a multi-allelic genetic coding locus comprising:

   (a) amplifying genomic DNA with a primer pair that spans a non-coding region sequence, said primer pair defining a DNA sequence which is in genetic linkage with said genetic coding locus and contains a sufficient

number of non-coding region sequence nucleotides to produce an amplified DNA sequence characteristic of said at least one haplotype;

(b) analyzing the amplified DNA sequence; and

(c) determining at least one haplotype of the multiallelic genetic coding locus.

14. The method of claim 13, wherein a single haplotype is determined.

15. The method of claim 13, wherein two or more haplotypes are determined.

16. The method of claim 13, wherein the genetic locus is an HLA locus.

17. The method of claim 13, wherein the at least one haplotype is associated with a genetic disease.

18. The method of claim 17, wherein the genetic disease is associated with variations in a regulatory or other untranslated region of the genetic locus.

19. (Amended) A method for determination of at least one haplotype of an HLA coding locus comprising:

(a) amplifying genomic DNA with a primer pair that spans a non-coding region sequence, said primer pair defining a DNA sequence which is in genetic linkage with said HLA coding locus;

(b) analyzing the amplified DNA sequence; and

(c) determining at least one haplotype of the HLA coding locus.

20. The method of claim 19, wherein a single haplotype is determined.

21. The method of claim 19, wherein two or more haplotypes are determined.

22. The method of claim 19, further comprising forensic testing.

23. The method of claim 22, further comprising:

(a) analyzing DNA from a crime scene sample;

(b) analyzing DNA from a sample of a suspected perpetrator of the crime; and

(c) comparing the haplotypes present in the crime scene sample and the suspected perpetrator sample.

24. The method of claim 19, further comprising paternity testing.

25. The method of claim 24, further comprising:

(i) analyzing DNA from an off-spring;

(ii) analyzing DNA from at least one suspected parent; and

(iii) comparing the haplotypes present in the offspring's DNA and in the suspected parent's DNA.

26. (New) The method of claim 1, wherein the haplotype is determined by detecting polymorphisms in coding and non-coding regions.

27. (New) The method of claim 1, wherein the non-coding region comprises an intervening sequence, a 5' untranslated sequence (5'-UTR), a 3'-UTR, a regulatory sequence or an intergenic sequence.

28. (New) The method of claim 13, wherein the non-coding region comprises an intervening sequence, a 5' untranslated sequence (5'-UTR), a 3'-UTR, a regulatory sequence or an intergenic sequence.

29. (New) The method of claim 19, wherein the haplotype is determined by detecting polymorphisms in coding and non-coding regions.

30. (New) The method of claim 19, wherein the non-coding region comprises an intervening sequence, a 5' untranslated sequence (5'-UTR), a 3'-UTR, a regulatory sequence or an intergenic sequence.

Remark

By this amendment, original claims 1, 13 and 19 have been amended. New claims 26-30 have been added. Claims 1-30 are presently pending in the case.

Support for the amendments may be found in the specification at least as follows. The amendment to claims 1, 13 and 19 to recite "genetic coding locus" or "HLA coding locus" is supported in the specification at least at pg. 11, lines 3-9, which defines a